Amendments to the Specification:

Please amend the paragraph [0040] column 1, on page 6, as follows:

The pellet obtained was suspended and sonicated in 50 mM Tris-HCl pH 7.0, 500 mM NaCl, 10% glycerol, 10 mM β-mercaptoethanol, 5 mM imidazole, and 0.1 mg/ml lysozyme, and the resulting lysate was separated into soluble and insoluble fractions by centrifugation. The fusion protein was purified using BD-~~Talon~~ TALON® cobalt-based affinity chromatography resin (BD-TALON® Metal Affinity Resin is a durable immobilized metal affinity chromatography [IMAC] resin that has a remarkable affinity and specificity for His-tagged proteins) (BD Biosciences Clontech, Palo Alto, CA) according to the protocol supplied by the manufacturer.

Please amend the paragraph [0037] column 2, on page 5, as follows:

The coding region of the *miox* cDNA in chromosome 4 (*miox4*, GenBank accession no. At4g26260) of *A. thaliana* was isolated by PCR and sequenced. Specific primers for the putative *miox* gene in chromosome 4 (*miox*4) were designed with *Nco*I and *Bam*HI sites added to the forward (MX4-5 CCCATGGCGATCTCTGTTGAG; SEQ ID NO:1) and reverse (MX4-3 CCGGATCCTCACCAC CTCAAG; SEQ ID NO:2) primers to facilitate sub-cloning. A 25 µl PCR reaction containing 3 µl of an *A. thaliana* mixed tissue cDNA library (CD4-7) from the Arabidopsis Biological Resource Center (ABRC, Columbus, OH) as template was performed with proofreading polymerase (*Pfu* Turbo DNA polymerase, Stratagene, La Jolla, CA). After denaturation at 94 °C for 5 min, amplification was performed by 30 cycles of 1 min at 94 °C, 1 min at 50 °C and 2 min at 72 °C, followed by 10 min at 72 °C. The 957 bp PCR fragment was cloned into the pGEM-T Easy vector (Promega, Madison, WI), amplified in *Escherichia coli* DH5α and sequenced in both directions with T7 and SP6 primers using the ABI PRISM BigDye Terminator Cycle Sequencing Kit (PE Applied Biosystems, Foster City, CA). A BLAST (Altschul *et al.*, 1997) search with the 957 bp PCR product revealed three changes at bases 233, 759 and 901 when compared to the published sequence. Two of those changes caused a substitution

at the amino acid level (Q_{78} to R and K_{300} to E, GenBank accession no. AY232552). The molecular mass based on the translated amino acid sequence for MIOX4 was calculated to be 37.061 Da with a theoretical pI of 4.83. The nucleic acid sequence (SEQ ID NO:3) and the amino acid sequence (SEQ ID NO:4) are given in **FIG. ~~3 and 4~~ 4 and 5**, respectively.